

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> NOVEL METHOD FOR GENE CLONING

<130> C1-001DP1PCT

<150> JP 1998-138652

<151> 1998-05-20

<150> JP 1998-279876

<151> 1998-10-01

<160> 39

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Peptide Linker Sequence

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

15

<210> 2

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1035)

<400> 2

atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg

48

Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro

1

5

10

15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga

96

Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg

20

25

30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro	35	40	45	144
ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys	50	55	60	192
ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg	65	70	75	240
ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys	85	90	95	288
tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val	100	105	110	336
ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser	115	120	125	384
aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr	130	135	140	432
aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp	145	150	155	480
ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys	165	170	175	528
cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met	180	185	190	576
tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe	195	200	205	624
cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val				672

210	215	220	
act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp			720
225	230	235	240
ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg			768
245	250	255	
tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp			816
260	265	270	
ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His			864
275	280	285	
gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser			912
290	295	300	
gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser			960
305	310	315	320
cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr			1008
325	330	335	
aat aaa gac gat gat aat att ctc ttc Asn Lys Asp Asp Asp Asn Ile Leu Phe			1035
340	345		
 <210> 3			
<211> 40			
<212> DNA			
<213> Artificial Sequence			
 <220>			
<223> Description of Artificial Sequence: "IL6R1", an artificially synthesized primer sequence			
 <400> 3			
ttcgaattcc caccatgctg gccgtcggtc gcgcgctgtct			
40			

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "IL6R2", an artificially synthesized primer sequence

<400> 4
ttcgaattcg aagagaatat tatcatcgac tttatt 36

<210> 5
<211> 768
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(768)

<220>
<223> Description of Artificial Sequence: a designed single chain Fv gene sequence

<400> 5
cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg 144
His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc 192
Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc 240
Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt 288

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc			336
Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly			
100	105	110	
agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt ggt ggt ggt			384
Ser Leu Val Thr Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly			
115	120	125	
tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc			432
Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser			
130	135	140	
ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc			480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser			
145	150	155	160
cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag			528
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys			
165	170	175	
gct cca aag ctg ctg atc tac acc tcc aga ctg cac tct ggt gtg			576
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val			
180	185	190	
cca agc aga ttc agc ggt agc ggt acc gac ttc acc ttc acc			624
Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr			
195	200	205	
atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag			672
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln			
210	215	220	
ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc			720
Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile			
225	230	235	240
aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccc cca tct gat			768
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp			
245	250	255	
<210> 6			
<211> 32			
<212> DNA			

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence

<400> 6

ggtgtcgact cccaggtcca actgcaggag ag

32

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence

<400> 7

ctcgtcacag ttcctcagg tggtgggtgt tc

32

<210> 8

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK3", an artificially synthesized primer sequence

<400> 8

gacatccaga tgaccaggag cccaaaggcgc ctgagcgc

38

<210> 9

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-C", an artificially synthesized primer sequence

<400> 9

gctgaattct tattatttat cgcatcgta tttgtagtca agtttatcag atggcgggaa

60

gat

63

<210> 10
<211> 9
<212> PRT

<400> 10
Met Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "LINK2", an artificially synthesized primer sequence

<400> 11
aaccaccacc acctgaggag actgtgacga ggct

34

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "LINK4", an artificially synthesized primer sequence

<400> 12
aggctgcttg ggctctgggt catctggatg tccga

35

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "TMT2", an artificially synthesized primer sequence

<400> 13
atcccgccgccc gcttattatt tatacgatc gtcttt

36

<210> 14

<211> 19
<212> PRT

<400> 14
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val Asp Ser

<210> 15
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "S-FLAG1", an artificially synthesized oligonucleotide sequence

<400> 15
aattccacc atggatgga gctgtatcat cctcttcttg gtagcaacag ctacagggtgt 60
cgactccgac tacaaagacg atgacgataa aggtaccgcg gccgcg 106

<210> 16
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "S-FLAG2", an artificially synthesized oligonucleotide sequence

<400> 16
gatccgcggc cgccgtacct ttatcgcat cgtcttcta gtccggatcg acacctgttag 60
ctgttgctac caagaagagg atgatacagc tccatccat ggtggg 106

<210> 17
<211> 2995
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (29)..(2839)

<400> 17
 gaattccgga catctagagg cagcgaacctt gtttccgatt catgtttat catttcttaa 60

tttcgtatgt tgggaacatc cctgcaag atg tca gca cca agg att tgg cta 112
 Met Ser Ala Pro Arg Ile Trp Leu
 1 5

gct caa gct ttg ctt ttt ttc acc act gaa tct ata ggt caa ctt 160
 Ala Gln Ala Leu Leu Phe Phe Leu Thr Thr Glu Ser Ile Gly Gln Leu
 10 15 20

ttg gaa ccg tgt ggt tac atc tac cct gaa ttt cca gtt gtc cag cgc 208
 Leu Glu Pro Cys Gly Tyr Ile Tyr Pro Glu Phe Pro Val Val Gln Arg
 25 30 35 40

ggc tcg aac ttc act gcc att tgt gtg ctg aag gag gct tgt ctg cag 256
 Gly Ser Asn Phe Thr Ala Ile Cys Val Leu Lys Glu Ala Cys Leu Gln
 45 50 55

cat tac tac gtg aat gcc agc tac atc gtg tgg aag acc aac cat gct 304
 His Tyr Tyr Val Asn Ala Ser Tyr Ile Val Trp Lys Thr Asn His Ala
 60 65 70

gct gtt ccc agg gag cag gtc act gtc atc aac aga acc acg tcc agt 352
 Ala Val Pro Arg Glu Gln Val Thr Val Ile Asn Arg Thr Thr Ser Ser
 75 80 85

gtc acg ttc aca gac gtg gtc ctc ccg agc gtg cag ctc acc tgc aac 400
 Val Thr Phe Thr Asp Val Val Leu Pro Ser Val Gln Leu Thr Cys Asn
 90 95 100

atc ctg tcc ttt ggg cag atc gag cag aat gtg tat gga gtc acc atg 448
 Ile Leu Ser Phe Gly Gln Ile Glu Gln Asn Val Tyr Gly Val Thr Met
 105 110 115 120

ctt tca ggc ttt cct cca gat aaa cct aca aat ttg act tgc att gtg 496
 Leu Ser Gly Phe Pro Pro Asp Lys Pro Thr Asn Leu Thr Cys Ile Val
 125 130 135

aat gag ggg aag aat atg ctg tgc cag tgg gac ccc gga agg gag act 544
 Asn Glu Gly Lys Asn Met Leu Cys Gln Trp Asp Pro Gly Arg Glu Thr
 140 145 150

tac ctt gaa aca aac tac act ttg aaa tca gag tgg gca aca gag aag 592
 Tyr Leu Glu Thr Asn Tyr Thr Leu Lys Ser Glu Trp Ala Thr Glu Lys

155	160	165	
ttt cct gat tgc cag tca aag cat ggc act tca tgt atg gtc agc tac Phe Pro Asp Cys Gln Ser Lys His Gly Thr Ser Cys Met Val Ser Tyr			640
170	175	180	
atg ccc acc tat tat gtc aac att gaa gtc tgg gtg gaa gca gag aat Met Pro Thr Tyr Tyr Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn			688
185	190	195	200
gcc ctt ggg aag gtc tcc tca gag tct atc aat ttt gac ccc gtg gat Ala Leu Gly Lys Val Ser Ser Glu Ser Ile Asn Phe Asp Pro Val Asp			736
205	210	215	
aaa gtg aaa ccc acc cca cca tat aat tta tca gtg acc aac tca gaa Lys Val Lys Pro Thr Pro Pro Tyr Asn Leu Ser Val Thr Asn Ser Glu			784
220	225	230	
gaa tta tcc agt ata tta aag cta tca tgg gtc agt tca ggg ctg ggc Glu Leu Ser Ser Ile Leu Lys Leu Ser Trp Val Ser Ser Gly Leu Gly			832
235	240	245	
ggt ctt tta gat cta aag tct gac atc caa tat agg acc aaa gat gcc Gly Leu Leu Asp Leu Lys Ser Asp Ile Gln Tyr Arg Thr Lys Asp Ala			880
250	255	260	
tca act tgg atc cag gtc cct ctt gaa gat aca atg tct cct cga act: Ser Thr Trp Ile Gln Val Pro Leu Glu Asp Thr Met Ser Pro Arg Thr			928
265	270	275	280
tcc ttc act gtg cag gac ctc aag cct ttt aca gaa tat gtg ttt agg Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg			976
285	290	295	
atc cgg tcc att aag gac agt ggg aag ggc tac tgg agt gac tgg agt Ile Arg Ser Ile Lys Asp Ser Gly Lys Gly Tyr Trp Ser Asp Trp Ser			1024
300	305	310	
gag gag gct agt ggg acc aca tac gaa gac aga cca tcc aga cca cca Glu Glu Ala Ser Gly Thr Thr Tyr Glu Asp Arg Pro Ser Arg Pro Pro			1072
315	320	325	
agt ttc tgg tat aag aca aat cca tcc cat ggg cag gaa tat aga tct Ser Phe Trp Tyr Lys Thr Asn Pro Ser His Gly Gln Glu Tyr Arg Ser			1120
330	335	340	

gta cgg ctc ata tgg aag gca ctg cct ctt tct gaa gcc aat ggg aaa Val Arg Leu Ile Trp Lys Ala Leu Pro Leu Ser Glu Ala Asn Gly Lys 345 350 355 360	1168
atc ttg gat tat gaa gtg att ctt acg cag tca aag tcc gtc tca caa Ile Leu Asp Tyr Glu Val Ile Leu Thr Gln Ser Lys Ser Val Ser Gln 365 370 375	1216
acg tac aca gtc act ggc aca gag ctg acc gtg aat ctc acc aat gac Thr Tyr Thr Val Thr Gly Thr Glu Leu Thr Val Asn Leu Thr Asn Asp 380 385 390	1264
cgc tat gtc gcg tct cta gca gca aga aac aag gtg ggc aaa tca gct Arg Tyr Val Ala Ser Leu Ala Ala Arg Asn Lys Val Gly Lys Ser Ala 395 400 405	1312
gca gct gtc ctc acc atc ccc agc ccc cac gtc aca gct gct tat tct Ala Ala Val Leu Thr Ile Pro Ser Pro His Val Thr Ala Ala Tyr Ser 410 415 420	1360
gta gtg aat ctt aaa gca ttt cca aaa gat aac ctg ctc tgg gtg gaa Val Val Asn Leu Lys Ala Phe Pro Lys Asp Asn Leu Leu Trp Val Glu 425 430 435 440	1408
tgg aca cct cca cct aaa ccc gtg agc aag tac atc tta gag tgg tgt Trp Thr Pro Pro Pro Lys Pro Val Ser Lys Tyr Ile Leu Glu Trp Cys 445 450 455	1456
gtg ttg tca gag aac gca ccc tgt gtt gaa gac tgg cag cag gaa gac Val Leu Ser Glu Asn Ala Pro Cys Val Glu Asp Trp Gln Gln Glu Asp 460 465 470	1504
gct acc gtg aat cggtt acc cac ttg aga gga cgc ctc ctg gag agc aag Ala Thr Val Asn Arg Thr His Leu Arg Gly Arg Leu Leu Glu Ser Lys 475 480 485	1552
tgc tat caa atc aca gta act ccc gta ttc gcc acg ggg ccc gga ggc Cys Tyr Gln Ile Thr Val Thr Pro Val Phe Ala Thr Gly Pro Gly Gly 490 495 500	1600
tct gag tcc ttg aag gcg tac ctc aaa caa gcc gct cct gcc aga gga Ser Glu Ser Leu Lys Ala Tyr Leu Lys Gln Ala Ala Pro Ala Arg Gly 505 510 515 520	1648
ccg act gtt cggtt aca aag aaa gtg ggg aaa aat gaa gct gtc tta gcg Pro Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Ala	1696

525	530	535	
tgg gac cag att cct gtg gac gac cag aat ggc ttc att aga aac tac Trp Asp Gln Ile Pro Val Asp Asp Gln Asn Gly Phe Ile Arg Asn Tyr			1744
540	545	550	
tcc ata tct tac aga acc agc gtg gga aag gag atg gtt gtg cat gtg Ser Ile Ser Tyr Arg Thr Ser Val Gly Lys Glu Met Val Val His Val			1792
555	560	565	
gat tct tct cac acg gag tac acg ctg tcc tct ctg agt agt gat acg Asp Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Ser Asp Thr			1840
570	575	580	
ttg tac atg gtc cga atg gcc gcg tac aca gat gaa ggt ggg aaa gat Leu Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp			1888
585	590	595	600
ggg ccg gaa ttc act ttt aca aca cca aag ttc gct caa gga gaa ata Gly Pro Glu Phe Thr Phe Thr Pro Lys Phe Ala Gln Gly Glu Ile			1936
605	610	615	
gaa gcc ata gtc gtg cct gtg tgc tta gcc ttc ctc ctg aca acc ctg Glu Ala Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu			1984
620	625	630	
ctg ggc gtc ttg ttc tgc ttt aac aaa cga gac cta att aaa aaa cac Leu Gly Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His			2032
635	640	645	
atc tgg cct aat gtt cct gat cct tcc aag agt cat att gcc cag tgg Ile Trp Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp			2080
650	655	660	
tca cct cac acc ccc cca agg cac aat ttt aac tcc aaa gat caa atg Ser Pro His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met			2128
665	670	675	680
tac tcg gac ggc aat ttc act gat gta agc gtt gtg gaa ata gaa gca Tyr Ser Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala			2176
685	690	695	
aac aac aag aag cct tgt cca gat gac ctg aag tcc gtg gac ctg ttc Asn Asn Lys Lys Pro Cys Pro Asp Asp Leu Lys Ser Val Asp Leu Phe			2224
700	705	710	

aag aag gag aaa gtg agt aca gaa ggg cac agc agt ggc atc ggg ggc Lys Lys Glu Lys Val Ser Thr Glu Gly His Ser Ser Gly Ile Gly Gly 715 720 725	2272
tct tca tgc atg tcc tcc tcc agg ccc agc atc tcc agc aac gag gag Ser Ser Cys Met Ser Ser Arg Pro Ser Ile Ser Ser Asn Glu Glu 730 735 740	2320
aat gag tct gct cag agc acc gcc agc acg gtc gag tac tcc act gtg Asn Glu Ser Ala Gln Ser Thr Ala Ser Thr Val Glu Tyr Ser Thr Val 745 750 755 760	2368
gtg cac agc ggc tac agg cac cag gtc ccg tcc gtg caa gtg ttc tca Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser 765 770 775	2416
agg tcc gag tcc acc cag ccc ctg cta gac tcg gag gag cgg cca gaa Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu 780 785 790	2464
gac ctg cag ctg gtg gat agt gta gac ggt ggg gat gag atc ttg ccc Asp Leu Gln Leu Val Asp Ser Val Asp Gly Gly Asp Glu Ile Leu Pro 795 800 805	2512
agg caa ccg tat ttc aag cag aac tgc agt cag cct gaa gcc tgt cca Arg Gln Pro Tyr Phe Lys Gln Asn Cys Ser Gln Pro Glu Ala Cys Pro 810 815 820	2560
gag att tca cat ttt gaa agg tca aac cag gtt ttg tcc ggc aat gag Glu Ile Ser His Phe Glu Arg Ser Asn Gln Val Leu Ser Gly Asn Glu 825 830 835 840	2608
gag gat ttt gtc aga ctg aag cag cag cag gtt tca gat cac att tct Glu Asp Phe Val Arg Leu Lys Gln Gln Val Ser Asp His Ile Ser 845 850 855	2656
cag ccc tat gga tcc gag caa cgg agg ctg ttt cag gaa ggc tct aca Gln Pro Tyr Gly Ser Glu Gln Arg Arg Leu Phe Gln Glu Gly Ser Thr 860 865 870	2704
gcg gat gct ctt ggc acg ggg gct gat gga cag atg gag aga ttt gaa Ala Asp Ala Leu Gly Thr Gly Ala Asp Gly Gln Met Glu Arg Phe Glu 875 880 885	2752
tct gtt gga atg gag acc aca att gat gaa gaa att ccc aaa agt tac Ser Val Gly Met Glu Thr Thr Ile Asp Glu Glu Ile Pro Lys Ser Tyr	2800

890	895	900
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ttg cca cag act gta aga caa ggt ggc tac atg ccg cag tgaaggactg Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln	2849
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905	910	915
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gctcctgaac ttcagcagga actgcaaaat aaagctaaag acgagtggct tcagatgaga	2909
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aacagtcctc actccctgaa gataggcatt gcctctaagg acaaagtac acctgggccg	2969
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tctccattcc agagtagctg gaattc	2995
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<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp1", an artificially synthesized primer sequence

<400> 18

cccaagcttg aattcacttt tacaaca	27
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<210> 19

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp3", an artificially synthesized primer sequence

<400> 19

tttgccggccg cgaattccag ctactctgg	29
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<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp2", an artificially synthesized primer sequence

<400> 20

cccaagctt aattcaaaaa acacatctgg ctt	33
<210> 21	
<211> 1662	
<212> DNA	
<213> Artificial Sequence	
 <220>	
<221> CDS	
<222> (11)..(1648)	
 <220>	
<223> Description of Artificial Sequence: "hPM1-BvGS3", a designed single chain Fv gene sequence	
 <400> 21	
gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca	49
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
1 5 10	
 gct aca ggt gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	97
Ala Thr Gly Val Asp Ser Gln Val Gln Leu Gln Ser Gly Pro Gly	
15 20 25	
 ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	145
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
30 35 40 45	
 tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	193
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
50 55 60	
 gga cga ggt ctt gag tgg att gga tac att agt tat gga atc aca	241
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
65 70 75	
 acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	289
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
80 85 90	
 agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	337
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
95 100 105	
 acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	385
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Ala Met	

110	115	120	125	
				433
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt				
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly				
130	135	140		
				481
ggt tcg ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg				
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met				
145	150	155		
				529
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc				
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr				
160	165	170		
				577
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac				
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr				
175	180	185		
				625
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc				
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser				
190	195	200	205	
				673
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt				
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly				
210	215	220		
				721
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct				
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala				
225	230	235		
				769
acc tac tac tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa				
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln				
240	245	250		
				817
ggg acc aag gtg gaa atc aaa tct aga ggt ggt ggt tcg ggt ggt				
Gly Thr Lys Val Glu Ile Lys Ser Arg Gly Gly Ser Gly Gly				
255	260	265		
				865
ggt ggt tcg ggt ggt ggc gga tcg gtc gac tcc cag gtc caa ctg cag				
Gly Gly Ser Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln				
270	275	280	285	
				913
gag agc ggt cca ggt ctt gtg aga cct agc cag acc ctg agc ctg acc				
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr				
290	295	300		

tgc acc gtg tct ggc tac tca att acc agc gat cat gcc tgg agc tgg Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp 305	310	315	961	
gtt cgc cag cca cct gga cga ggt ctt gag tgg att gga tac att agt Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser 320	325	330	1009	
tat agt gga atc aca acc tat aat cca tct ctc aaa tcc aga gtg aca Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr 335	340	345	1057	
atg ctg aga gac acc agc aag aac cag ttc agc ctg aga ctc agc agc Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser 350	355	360	365	1105
gtg aca gcc gcc gac acc gcg gtt tat tat tgt gca aga tcc cta gct Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala 370	375	380	1153	
cgg act acg gct atg gac tac tgg ggt caa ggc agc ctc gtc aca gtc Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val 385	390	395	1201	
tcc tca ggt ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt ggc gga Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly 400	405	410	1249	
tcg gac atc cag atg acc cag agc cca agc agc ctg agc gcc agc gtg Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val 415	420	425	1297	
ggt gac aga gtg acc atc acc tgt aga gcc agc cag gac atc agc agt Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser 430	435	440	445	1345
tac ctg aat tgg tac cag cag aag cca gga aag gct cca aag ctg ctg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu 450	455	460	1393	
atc tac tac acc tcc aga ctg cac tct ggt gtg cca agc aga ttc agc Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser 465	470	475	1441	
ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln			1489	

480	485	490	
cca gag gac atc gct acc tac tac tgc caa cag ggt aac acg ctt cca			1537
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro			
495	500	505	

tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct			1585
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala			
510	515	520	525

gca cca tct gtc ttc atc ttc ccg cca tct gat aag ctt gac tac aaa			1633
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Lys Leu Asp Tyr Lys			
530	535	540	

gac gat gac gat aaa taataaggccg			1662
Asp Asp Asp Asp Lys			
545			

<210> 22

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "BvGS3", an artificially synthesized primer sequence

<400> 22

ggagtgcacc gatccgccac cacccgaacc accaccaccc gaaccaccac caccttgat 60

ttccacccgt

72

<210> 23

<211> 780

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(780)

<220>

<223> Description of Artificial Sequence: "shPM1(ΔEL)", a designed single chain Fv gene sequence

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
 Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
 35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
 Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
 50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240
 Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
 65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288
 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn
 85 90 95

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt 336
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg 384
 Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp
 115 120 125

ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt 432
 Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 130 135 140

ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc 480
 Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 145 150 155 160

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 528
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 165 170 175

aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag 576
 Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys

180	185	190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His 195	200	205	624
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 210	215	220	672
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr 225	230	235	720
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys 245	250	255	768
gtg gaa atc aaa Val Glu Ile Lys 260			780
<210> 24			
<211> 321			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)..(321)			
<400> 24			
cga act gtg gct gca cca tct gtc atc ttc ccg cca tct gat gag Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu 1	5	10	48
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe 20	25	30	96
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln 35	40	45	144
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc			192

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95

ccc gtc aca aag agc ttc aac agg gga gag tct 321
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser
 100 105

<210> 25
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(363)

<400> 25
 gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cg_g gag: 48
 Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu
 1 5 10 15

cag ctg aac ctg cg_g gag tcg gcc acc atc acg tgc ctg gtg acg ggc 96
 Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly
 20 25 30

ttc tct ccc gc_g gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc 144
 Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro
 35 40 45

ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag 192
 Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln
 50 55 60

gcc cca ggc cg_g tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag 240
 Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu
 65 70 75 80

gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc cat gag gcc ctg 288
Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala His Glu Ala Leu
85 90 95

ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc gag ggg gag 336
 Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Glu Gly Glu
 100 105 110

gtg agc gcc gac gag gag ggc ttt gag 363
Val Ser Ala Asp Glu Glu Gly Phe Glu
115 120

<210> 26

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1101)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa", a designed single chain Fv gene sequence

<400> 26

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
 Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn

65	70	75	80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn				288
85	90		95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val				336
100	105		110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp				384
115	120		125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly				432
130	135		140	
ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg acc cag agc Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln Ser				480
145	150	155	160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys				528
165	170		175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys				576
180	185		190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His				624
195	200		205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe				672
210	215		220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc fac tac Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr				720
225	230	235	240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys				768
245	250		255	

gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg		816	
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
260	265	270	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg		864	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
275	280	285	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat		912	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
290	295	300	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac		960	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
305	310	315	320
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa		1008	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
325	330	335	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag		1056	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
340	345	350	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tct		1101	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser			
355	360	365	

<210> 27
<211> 1143
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1143)

<220>
<223> Description of Artificial Sequence: "shPM1-MCH4", a designed single chain Fv gene sequence

<400> 27
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1	5	10	15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg				96
20	25		30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile				144
35	40		45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly				192
50	55		60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn				240
65	70	75		80
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn				288
85	90		95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gac acc gac gtt Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val				336
100	105		110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp				384
115	120		125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly				432
130	135		140	
ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg acc cag agc Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln Ser				480
145	150	155		160
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys				528
165	170		175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys				576
180	185		190	

cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac		624	
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His			
195	200	205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc		672	
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe			
210	215	220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac		720	
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr			
225	230	235	240
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag		768	
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys			
245	250	255	
gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca		816	
Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro			
260	265	270	
cca gcc cgg gag cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc		864	
Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys			
275	280	285	
ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag		912	
Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln			
290	295	300	
agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc acc ggc cca atg		960	
Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met			
305	310	315	320
cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc		1008	
Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr			
325	330	335	
gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc		1056	
Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala			
340	345	350	
cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc		1104	
His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser			
355	360	365	
acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag		1143	
Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu			

370

375

380

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "EF-1", an artificially synthesized primer sequence

<400> 28

cagacagtgg ttcaaagt

18

<210> 29

<211> 107

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-02", an artificially synthesized primer sequence

<400> 29

aaagcggccg cttattatcc atcgcatcg tctttgttgtt ctgaagctt gatttccacc 60

ttggccctt ggccgaacgt gtatggtaaa gtatccct gttggca

107

<210> 30

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1557)

<220>

<223> Description of Artificial Sequence: "shPM1(ΔEL)-BvGS3", a designed single chain Fv gene sequence

<400> 30

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt		48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly		
1	5	10
		15
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga		96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg		
20	25	30
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att		144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile		
35	40	45
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt		192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly		
50	55	60
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat		240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn		
65	70	75
		80
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac		288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn		
85	90	95
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt		336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val		
100	105	110
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg		384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp		
115	120	125
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt		432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly		
130	135	140
ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg acc cag agc		480
Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln Ser		
145	150	155
		160
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt		528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys		
165	170	175
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag		576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys		

180	185	190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac 624			
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His			
195	200	205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc 672			
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe			
210	215	220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac 720			
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr			
225	230	235	240
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag 768			
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys			
245	250	255	
gtg gaa atc aaa ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt 816			
Val Glu Ile Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly			
260	265	270	
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 864			
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly			
275	280	285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc 912			
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly			
290	295	300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct 960			
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro			
305	310	315	320
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca 1008			
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr			
325	330	335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc 1056			
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr			
340	345	350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac 1104			
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp			
355	360	365	

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg		1152	
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met			
370	375	380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt		1200	
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly			
385	390	395	400
ggt tcg ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg		1248	
Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Gln Met			
405	410	415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc		1296	
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr			
420	425	430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac		1344	
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr			
435	440	445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc		1392	
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser			
450	455	460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt		1440	
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly			
465	470	475	480.
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct		1488	
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala			
485	490	495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa		1536	
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln			
500	505	510	
ggg acc aag gtg gaa atc aaa		1557	
Gly Thr Lys Val Glu Ile Lys			
515			

<210> 31
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa1", an artificially synthesized primer sequence

<400> 31

ccgccccatctg atgagcagtt gaaatctgg

29

<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa2", an artificially synthesized primer sequence

<400> 32

ttatttatcg tcatcgtctt tgtagtcaag ctttagactct cccctgttga agct

54

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-K", an artificially synthesized primer sequence

<400> 33

ttcaactgct catcagatgg cgggaaagat

29

<210> 34

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1878)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa-BvGS3", a designed single chain Fv gene sequence

<400> 34

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1	5	10	15
---	---	----	----

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
 Val Asp Ser Gln Val Gln Leu Gln Ser Gly Pro Gly Leu Val Arg
 20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
 35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
 Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
 50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240
 Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
 65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288
 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn
 85 90 95

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt 336
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg 384
 Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp
 115 120 125

ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt tcg ggt 432
 Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 130 135 140

ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc 480
 Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 145 150 155 160

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 528
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 165 170 175

aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	180	185	190	576	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	195	200	205	624	
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	210	215	220	672	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	225	230	235	240	720
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	245	250	255	768	
gtg gaa atc aaa ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt Val Glu Ile Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly	260	265	270	816	
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly.	275	280	285	864	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	290	295	300	912	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	305	310	315	960	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	325	330	335	1008	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	340	345	350	1056	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac				1104	

Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp				
355	360	365		
acc gcg gtt tat tat tgt gca aga tcc cta gct cggt act acg gct atg				1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met				
370	375	380		
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt				1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly				
385	390	395	400	
ggt tcg ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg				1248
Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Gln Met				
405	410	415		
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc				1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr				
420	425	430		
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac				1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr. Leu Asn Trp Tyr				
435	440	445		
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc				1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser				
450	455	460		
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt				1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly				
465	470	475	480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct				1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala				
485	490	495		
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa				1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln				
500	505	510		
ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc				1584
Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe				
515	520	525		
atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt				1632
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val				
530	535	540		

gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg 1680
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 545 550 555 560

aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca 1728
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 565 570 575

gag cag gac agc aag gac acc tac agc ctc agc agc acc ctg acg 1776
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 580 585 590

ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc 1824
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 595 600 605

acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga 1872
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 610 615 620

gag tct 1878
 Glu Ser
 625

<210> 35

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "MCH4-1", an artificially synthesized primer sequence

<400> 35

gtggaaatca aagtggccct gcacaggcc

29

<210> 36

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "MCH4-2.1", an artificially synthesized primer sequence

<400> 36
tagtcaagct tctcaaattcc ctcttcgtcg ggcgtaacct ctccttcgggt ggacttgtcc 60
acggtcct 68

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "SCP-Mu", an artificially synthesized primer sequence

<400> 37
tgcaggcca ctttgatttc caccttggt 29

<210> 38
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: "MCH4-2.2", an artificially synthesized primer sequence

<400> 38
aaagcggccg cttattatcc atcgtcatcg tctttgtagt caagcttctc aaa 53

<210> 39
<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1920)

<220>
<223> Description of Artificial Sequence: "shPM1-MCH4-BvGS3", a designed single chain Fv gene sequence

<400> 39

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt			48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga			96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg			
20	25	30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att			144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile			
35	40	45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt			192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly			
50	55	60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat			240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn			
65	70	75	80
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac			288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn			
85	90	95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt			336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val.			
100	105	110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg			384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp			
115	120	125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt			432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly			
130	135	140	
ggt ggt ggt tcg ggt ggc gga tcg gac atc cag atg acc cag agc			480
Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser			
145	150	155	160
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt			528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys			
165	170	175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag			576

Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys				
180	185	190		
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624			
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His				
195	200	205		
tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc	672			
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe				
210	215	220		
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720			
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr				
225	230	235	240	
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768			
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys				
245	250	255		
gtg gaa atc aaa ggt ggt ggt tcg ggt ggt ggt tcg ggt ggt	816			
Val Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly				
260	265	270		
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864			
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly				
275	280	285		
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912			
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly				
290	295	300		
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960			
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro				
305	310	315	320	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008			
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr				
325	330	335		
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056			
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr				
340	345	350		
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104			
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp				
355	360	365		

acc gcg gtt tat tat tgt gca aga tcc cta gct cggt act acg gct atg Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met 370 375 380	1152
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly 385 390 395 400	1200
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Gln Met 405 410 415	1248
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr 420 425 430	1296
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr 435 440 445	1344
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser 450 455 460	1392
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly 465 470 475 480	1440
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala 485 490 495	1488
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln 500 505 510	1536
ggg acc aag gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac Gly Thr Lys Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr 515 520 525	1584
ttg ctg cca cca gcc cgg gag cag ctg aac ctg cgc gag tcg gcc acc Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr 530 535 540	1632
atc acg tgc ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag	1680

Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln				
545	550	555	560	
tgg atg cag agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc agc				1728
Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser				
565	570	575		
gcc cca atg cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc				1776
Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser				
580	585	590		
atc ctg acc gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc				1824
Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr				
595	600	605		
tgc gtg gcc cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg				1872
Cys Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val				
610	615	620		
gac aag tcc acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag				1920
Asp Lys Ser Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu				
625	630	635	640	